

DR N-PSDB; AAQ96297.
 XX DNA encoding monocyte chemo-attractant protein-1 receptor - used partic.
 PT for identifying antagonists and for treating diseases characterised by
 PT monocyte infiltrates.
 XX
 PS Claim 2; Fig 1; 84pp; English.
 CC To identify and clone new members of the chemokine receptor gene family,
 CC degenerate oligo primers were designed corresp. to the conserved
 CC sequences R79167 in the second and R79168 in the third transmembrane
 CC domains of the MIP-1alpha/RANTES receptor, the IL-8 receptors and the
 CC HUMSIRs orphan receptor (Genbank Accession #99293). The degenerate oligo
 CC incorporating EcoRI and XhoI sites at their 5' ends are Q96299 and
 CC Q96300. Amplification of cDNA derived from MM6 cells with the primers
 CC yielded a number of PCR products. One cDNA appeared to encode a novel
 CC protein. To obtain a full-length version of this clone, a MM6 cDNA
 CC library was constructed in pPROG and probed with the PCR product. A 2.1
 CC kb cDNA clone was obtd. Analysis of additional clones in the MM6 cDNA
 CC library revealed a second sequence that was identical to the 2.1 kb cDNA
 CC transmembrane domain but contained a different cytoplasmic tail. The
 CC second sequence appears to represent alternative splicing of the carboxyl
 CC -terminal tail of the MCP-1R protein. The two sequences are denoted MCP-
 CC 1RA and MCP-1RB (see Q96297/R79165 & Q96298/R79166). Active mature MCP-
 CC 1RA has a predicted mol. wt. of about 42,000 daltons. MCP-1RB has a mol.
 CC wt. of about 41,000 daltons. (Updated on 25-MAR-2003 to correct PN
 CC field.)
 XX
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 Query Match 100.0%; Score 1970; DB 2; Length 374;
 Best Local Similarity 100.0%; Pred. No. 5.1e-215;
 Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DB 121 HIGYFGGIFFIILLTIDRYLAIVHAFALKARTVTFGVTSVITWLVAFAVPGIIFTK 180
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 RESULT 2
 AAG80107
 ID AAG80107 standard; protein; 374 AA.
 XX
 AC AAG80107;
 XX
 DT 17-JAN-2002 (first entry)
 XX
 DE Human CCR2a protein.

XX Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection;
 KW inflammation; autoimmune disease; metastasis; bronchial asthma; lupus;
 KW chronic bowel inflammation; rheumatoid arthritis; cytostatic;
 KW antineoplastic; antineoplastic; immunosuppressive; dermatological;
 KW antineoplastic; antineoplastic.
 XX
 OS Homo sapiens.
 XX
 PN WO200172830-A2.
 XX
 PD 04-OCT-2001.
 XX
 PF 02-APR-2001; 2001WO-EP003708.
 XX
 PR 31-MAR-2000; 2000DE-01016013.
 XX
 XX (IIPP-) IFF PHARM GMBH.
 PA (FORS/) FORSMANN U.
 XX
 PI Forssmann W, Adermann K, Heltland A, Spodsberg N;
 XX
 DR WPI; 2001-626256/72.
 XX
 PT Diagnostic agent containing two or more receptor-specific ligands, useful
 PT for detecting tumors, inflammation etc., also therapeutic use of ligand
 PT inhibitors.
 XX
 PS Disclosure; Page 9; 26pp; German.
 XX
 CC This invention describes a novel diagnostic agent (A) comprising at least
 CC two different ligands (I) for receptors (II) that are implicated in
 CC disease. (A) are used for the diagnosis of tumors (especially colorectal
 CC or prostatic), organ rejection, inflammation and autoimmune diseases.
 CC Also inhibitors of (I) are used therapeutically against tumors (and their
 CC metastases), inflammation (particularly bronchial asthma or chronic bowel
 CC inflammation), or autoimmune diseases (rheumatoid arthritis or lupus),
 CC where the (cardio)vascular, lymphatic, respiratory, nervous, digestive,
 CC endocrine, motor or urogenital systems or skin are affected, and bone
 CC marrow diseases. The products of the invention are chemokine derivatives
 CC which have cytostatic, antiinflammatory, antineoplastic,
 CC immunosuppressive, dermatological, antineoplastic, antineoplastic.
 CC Chemokines act on specific tumor and inflammatory cells through a
 CC combination of chemokine receptors (CR), which control migration and
 CC proliferation of these cells. AAG80045-AAG80128 represent human chemokine
 CC fragments used to illustrate the method of the invention
 CC
 XX
 SQ Sequence 374 AA:
 Query Match 100.0%; Score 1970; DB 4; Length 374;
 Best Local Similarity 100.0%; Pred. No. 5.1e-215;
 Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MISTSRSRIRNTNSGSEVTTFFDYDYGAPCHKEDVKGQGLPPLYSLVIFGFVGN 60
 DB 1 MISTSRSRIRNTNSGSEVTTFFDYDYGAPCHKEDVKGQGLPPLYSLVIFGFVGN 60
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 QY 241 AVRVIETIMIVFLFMTPNIVILNTFOEFGLSNCESTSQDDATQVTEITLGMHCCI 300
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OM protein - protein search, using SW model

Run on: November 1, 2005, 21:10:05 ; Search time 43 Seconds

(Withou alignments)
649,273 Million cell updates/sec

Title: US-10-791-592-2

Perfect score: 1970

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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4	1970	100.0	374	4 US-09-625-573-2	Sequence 2, Appl1
5	1970	100.0	374	5 PCT-US95-00476-2	Sequence 2, Appl1
6	1970	100.0	374	4 US-09-949-016-11222	Sequence 11222, A
7	1823	92.5	344	3 US-08-466-943D-9	Sequence 9, Appl1
8	1823	92.5	344	4 US-09-502-784A-9	Sequence 9, Appl1
9	1727.5	87.7	329	4 US-09-502-783A-9	Sequence 9, Appl1
10	1727.5	87.7	329	4 US-09-339-912A-9	Sequence 9, Appl1
11	1727.5	87.7	329	4 US-09-195-662A-9	Sequence 9, Appl1
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19	1651.5	83.8	377	4 US-09-949-016-11221	Sequence 11221, A
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25	1614.5	82.0	360	3 US-09-045-583-51	Sequence 51, Appl1
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27	1589.5	80.7	347	1 US-08-461-244-3	Sequence 3, Appl1

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42	1224	62.1	352	4 US-08-771-276-20	Sequence 20, Appl1
43	1224	62.1	352	4 US-09-939-226B-5	Sequence 5, Appl1
44	1224	62.1	352	4 US-09-195-662A-2	Sequence 2, Appl1
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ALIGNMENTS

RESULT 1

US-08-450-393A-2

Sequence 2, Appl1

Patent No. 5707815

GENERAL INFORMATION:

APPLICANT: Chao, Israel

TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT

TITLE OF INVENTION: PROTEIN RECEPTORS

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESS: Cooley Godward Castro Huddleson & Tatum

STREET: 5 Palo Alto Square

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94306-2155

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/450,393A

FILING DATE: May 25, 1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Caert, Luann

REGISTRATION NUMBER: 31,822

REFERENCE/DOCKET NUMBER: UCAL-237/02US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-843-5165

TELEFAX: 415-8857-0663

TELEX: 380816COOLEYPA

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 374 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-450-393A-2

Query Match

Best Local Similarity 100.0%; Score 1970; DB 1; Length 374;

Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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28	1236	62.7	352	3 US-09-517-605-5	Sequence 5, Appl1
29	1234	62.6	354	3 US-08-724-984A-2	Sequence 2, Appl1
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RESULT 1

US-08-450-393A-2

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US-08-450-393A-2

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RESULT 2

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; Patent No. 6132987
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; APPLICANT: Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESSES:
; ADDRESSES: Cooley Godward Castro Huddleson & Tatum
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,669
; FILING DATE: May 25, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Neelley, Richard
; REGISTRATION NUMBER: 30,092
; REFERENCE/DOCKET NUMBER: UCAL-237/01US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5000
; TELEFAX: 415-857-0663
; TELEX: 380816COOLEYPA
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-446-669-2

Query Match 100.0%; Score 1970; DB 3; Length 374;
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Qy 181 COKEDSVYVCGPYFPRGMNPHITMRNIGLVPLLIWVCSSGILKTLRCRNEKKRR 240
Db 181 COKEDSVYVCGPYFPRGMNPHITMRNIGLVPLLIWVCSSGILKTLRCRNEKKRR 240
Qy 241 AVRVIETIMIVFLFWTPYNIIVLLNTFOEFGLSNCESTSOLDQATQVTEITLGMTHCCI 300
Db 241 AVRVIETIMIVFLFWTPYNIIVLLNTFOEFGLSNCESTSOLDQATQVTEITLGMTHCCI 300
Qy 301 NPIIYAFVGEKPRSLFHIALGCRIPLOKPVCGGPGVRPGKXVKTTOGLDGRGKXSI 360
Db 301 NPIIYAFVGEKPRSLFHIALGCRIPLOKPVCGGPGVRPGKXVKTTOGLDGRGKXSI 360
Qy 361 GRAPEASLODKEGA 374
Db 361 GRAPEASLODKEGA 374

RESULT 3

US-10-039-659A-14
; Sequence 14, Application US/10039659A
; Patent No. 6723520
; GENERAL INFORMATION:
; APPLICANT: Wang, Wei
; APPLICANT: Gish, Kurt C.
; APPLICANT: Vicari, Thomas J.
; APPLICANT: Zlocnik, Albert
; TITLE OF INVENTION: Antibodies that bind chemokine TECK
; FILE REFERENCE: DX0589K1B US
; CURRENT APPLICATION NUMBER: US/10/039,659A
; CURRENT FILING DATE: 2002-01-03
; PRIOR APPLICATION NUMBER: US 08/887,977
; PRIOR FILING DATE: 1997-07-03
; PRIOR APPLICATION NUMBER: US 60/021,664
; PRIOR FILING DATE: 1996-07-05
; PRIOR APPLICATION NUMBER: US 60/028,329
; PRIOR FILING DATE: 1996-10-11
; PRIOR APPLICATION NUMBER: US 60/048,593
; PRIOR FILING DATE: 1997-06-04
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 14
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-039-659A-14

Query Match 100.0%; Score 1970; DB 4; Length 374;
Best Local Similarity 100.0%; Pred. No. 4,3e-150;
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 M1STSRSRFRINTNBSGSEVTTFFDYDYGAPCHKEDVKQIGALLPPLYSLVIFGPGVN 60
|||||
Db 1 M1STSRSRFRINTNBSGSEVTTFFDYDYGAPCHKEDVKQIGALLPPLYSLVIFGPGVN 60
Qy 61 MLVVLILNCKKLCJTDIYLLNLAIISDLFLITLPLMAHSAANEMVFGNACKLFTGLY 120
Db 61 MLVVLILNCKKLCJTDIYLLNLAIISDLFLITLPLMAHSAANEMVFGNACKLFTGLY 120
Qy 121 HIGYFGGIFPIILLTIDRYLAIVHAVPALKARTVTFGVVTSVITWLVAVFASVPGIIFPK 180
Db 121 HIGYFGGIFPIILLTIDRYLAIVHAVPALKARTVTFGVVTSVITWLVAVFASVPGIIFPK 180

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OM protein - protein search, using SW model

Run on: November 1, 2005, 21:08:32 ; Search time 40 Seconds

(without alignments)
899,627 Million cell updates/sec

Title: US-10-791-592-2

Perfect score: 1970

Sequence: 1 M1STSRSRFRINTNESGEVY.....GKGSIGRAPEASLDQKEGA 374

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: PIR 79: *
2: PIR: *
3: PIR: *
4: PIR: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1970	100.0	374	2 I38450	chemokine (C-C) re
2	1651.5	83.8	360	2 UC2443	chemokine (C-C) re
3	1224	62.1	352	2 A43113	chemokine (C-C) re
4	967.5	49.1	355	2 A45177	chemokine (C-C) re
5	960	48.7	359	2 I49341	MIP-1 alpha receptor
6	902.5	45.8	355	2 I49339	macrophage inflam
7	890.5	45.2	355	2 G02436	chemokine (C-C) re
8	833	42.3	360	2 UC4587	chemokine (C-C) re
9	831.5	42.2	360	2 A57160	chemokine (C-C) re
10	794.5	40.3	363	2 S55594	G protein-coupled
11	731	37.1	356	2 I49340	MIP-1 alpha recept
12	723	36.7	355	2 UC5067	G protein-coupled
13	704.5	35.8	354	2 I58186	probable G protein
14	698	35.4	355	2 UC4304	orphan G protein-c
15	644.5	32.7	344	2 UC5942	chemokine receptor
16	584	29.6	378	2 B55735	lymphocyte-specifi
17	575.5	29.2	378	2 A55735	G protein-coupled
18	570	28.9	378	2 A45680	G protein-coupled
19	554.5	28.1	369	2 UC5068	G protein-coupled
20	541.5	27.5	360	2 A53611	interleukin-8 rece
21	537	27.3	359	2 A48921	interleukin-8 rece
22	530.5	26.9	353	2 G00048	fusin (LESTRA) - c
23	529.5	26.9	355	2 S28787	neuropeptide Y/pep
24	529.5	26.9	355	2 JQ1231	interleukin-8 rece
25	528	26.8	352	2 A53752	neuropeptide Y/pep
26	526	26.7	358	2 A53752	interleukin-8 rece
27	524.5	26.6	357	2 UC0349	interferon-inducib
28	524.5	26.6	350	2 A39445	interleukin-8 rece
29	523	26.5	356	2 S42096	interleukin-8 rece

30	519	26.3	333	2 I65989	G protein-coupled
31	484	24.6	350	2 JN0621	G protein-coupled
32	480	24.4	359	2 A42656	angiotensin II rec
33	479.5	24.3	374	2 S42628	G protein-coupled
34	475	24.1	359	2 I51372	angiotensin II rec
35	473	24.0	359	2 UC2134	angiotensin II rec
36	472	24.0	359	2 JH0621	angiotensin II rec
37	471	23.9	359	2 S15403	angiotensin II rec
38	471	23.9	359	2 JQ1516	angiotensin II rec
39	469	23.8	359	2 UC1104	angiotensin II rec
40	468	23.8	359	2 S44425	angiotensin II rec
41	465	23.6	359	2 UC1194	angiotensin II rec
42	465	23.6	374	2 S32785	G protein-coupled
43	464	23.6	359	2 A48857	angiotensin II rec
44	461.5	23.4	372	2 S26657	G protein-coupled
45	460.5	23.4	327	2 S56162	MDCK15 protein - h

ALIGNMENTS

RESULT 1

I38450
chemokine (C-C) receptor 2, splice form A - human
N:Alternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte che
C:Species: Homo sapiens (man)
C>Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 09-Jul-2004
C/Accession: I38450
R:Charo, I.F.; Myers, S.J.; Herman, A.; Francis, C.; Connolly, A.J.; Coughlin, S.R.
Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994
A:Title: Molecular cloning and functional expression of two monocyte chemoattractant pr
A:Reference number: A53477; PMID:94195821; PMID:8146186
A/Accession: I38450
A/Status: preliminary
A/Molecule type: mRNA
A:Residues: 1-374 <RES>
A:Cross-references: UNIPROT:P41597; EMBL:U03882; NID:G472555; PIDN:AAA19119.1; PID:G472
C:Gene: GDB:CMKBR2
A:Cross-references: GDB:337364; OMIM:601267
A:Map position: 3p21-3p21
C:Superfamily: vertebrate rhodopsin
C:Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembra
F:44-68/Domain: transmembrane #status predicted <TM1>
F:79-99/Domain: transmembrane #status predicted <TM2>
F:115-136/Domain: transmembrane #status predicted <TM3>
F:154-178/Domain: transmembrane #status predicted <TM4>
F:208-226/Domain: transmembrane #status predicted <TM5>
F:244-265/Domain: transmembrane #status predicted <TM6>
F:292-309/Domain: transmembrane #status predicted <TM7>
F:14/Binding site: carboxylate (Asn) (covalent) #status predicted
F:32-277,113-190/Disulfide bonds: #status predicted

Query Match 100.0%; Score 1970; DB 2; Length 374;
Best Local Similarity 100.0%; Pred. No. 1e-164;

Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	M1STSRSRFRINTNESGEVYTFPDYDYGAPCHKFPVKQIGAOQLPPLSLVIFGVGN 60
DB	1	M1STSRSRFRINTNESGEVYTFPDYDYGAPCHKFPVKQIGAOQLPPLSLVIFGVGN 60
QY	61	MLVVLILNCKKLCITDYLNLALSDLLFTLPLMAHSANENVPFGAMKLTGLY 120
DB	61	MLVVLILNCKKLCITDYLNLALSDLLFTLPLMAHSANENVPFGAMKLTGLY 120
QY	121	HIGYFGIFPIILLTIDRYLAIVHAFALKARTVFGVTSVITWVAVPASVGIIFTK 180
DB	121	HIGYFGIFPIILLTIDRYLAIVHAFALKARTVFGVTSVITWVAVPASVGIIFTK 180
QY	181	CKEDSVYVCGPFPFGMNFHTIMNIIIGLVPLIMVTCVSGIKTLRCNEKKRR 240
DB	181	CKEDSVYVCGPFPFGMNFHTIMNIIIGLVPLIMVTCVSGIKTLRCNEKKRR 240

QY 241 AVRVIPTIMIVFLFWPTPNIVILNTFOEFGLSNCESTSQLDQATQVTEITLGMTHCCI 300
 DB 241 AVRVIPTIMIVFLFWPTPNIVILNTFOEFGLSNCESTSQLDQATQVTEITLGMTHCCI 300
 QY 301 NPITIAFVGEKRRSLFHIALGRIAPLQKPVCGPGVPRGKVKVKTTOGLDGRGKSKI 360
 DB 301 NPITIAFVGEKRRSLFHIALGRIAPLQKPVCGPGVPRGKVKVKTTOGLDGRGKSKI 360
 QY 361 GRAPEASLQDKEGA 374
 DB 361 GRAPEASLQDKEGA 374

RESULT 2

JC2443
 chemokine (C-C) receptor 2, splice form B - human
 N:Alternate names: C-C CR-2; monocyte chemoattractant protein 1 receptor; monocyte chemokine
 C:Species: Homo sapiens (man)
 C>Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #ext_change 09-Jul-2004
 C:Accession: JC2443; 138463
 R:Yamagami, S.; Tokuda, Y.; Ishii, K.; Tanaka, H.; Endo, N.
 Biochem. Biophys. Res. Commun. 202, 1156-1162, 1994
 A>Title: cDNA cloning and functional expression of a human monocyte chemoattractant prot
 A:Reference number: JC2443; MUID:94324942; PMID:8048929
 A:Accession: JC2443
 A:Molecule type: mRNA
 A:Residues: 1-360 <YAM>
 A:Cross-references: UNIPROT:P41597; DDBJ:D29984; NID:G531246; PID:BA06253.1; PID:G5312
 R:Chato, I.F.; Myers, S.J.; Herman, A.; Francis, C.; Connolly, A.J.; Coughlin, S.R.
 Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994
 A>Title: Molecular cloning and functional expression of two monocyte chemoattractant pro
 A:Reference number: A53477; MUID:94195821; PMID:8146186
 A:Accession: I38463
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-360 <RES>
 A:Cross-references: EMBL:U03905; NID:9472557; PID:AAA19120.1; PID:9472558
 C:Genetics:
 A:Gene: GDB:CMKBR2
 A:Map position: 3p21-3p21
 A:Cross-references: GDB:337364; OMIM:601267
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembran
 F:43-70/Domain: transmembrane #status predicted <TM1>
 F:81-100/Domain: transmembrane #status predicted <TM2>
 F:115-136/Domain: transmembrane #status predicted <TM3>
 F:154-176/Domain: transmembrane #status predicted <TM4>
 F:207-226/Domain: transmembrane #status predicted <TM5>
 F:244-268/Domain: transmembrane #status predicted <TM6>
 F:287-309/Domain: transmembrane #status predicted <TM7>
 F:14/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:113-190/Disulfide bonds: #status predicted

Query Match 83.8%; Score 1651.5; DB 2; Length 360;
 Best Local Similarity 95.5%; Pred. No. 7.1e-137;
 Matches 319; Conservative 3; Mismatches 5; Indels 7; Gaps 3;

QY 1 MSTSRSRFRNTNSESGETTFFPDYAPCHKPFVKVIGAGQLPPLSLVFIKGFVN 60
 DB 1 MSTSRSRFRNTNSESGETTFFPDYAPCHKPFVKVIGAGQLPPLSLVFIKGFVN 60
 QY 61 MLVLLINCKKLCITDIYLLNLASDLLFLITPLMAHSANENVFQNAKCKFTGLY 120
 DB 61 MLVLLINCKKLCITDIYLLNLASDLLFLITPLMAHSANENVFQNAKCKFTGLY 120
 QY 121 HIGYRGIFPIILLTDRLVLAHVAFALKARTVFGVTSVITWLVAVFASVPGIIFPK 180
 DB 121 HIGYRGIFPIILLTDRLVLAHVAFALKARTVFGVTSVITWLVAVFASVPGIIFPK 180
 QY 181 CGKEDSVVYCGPYFPGMNPFTIMNIIIGVLPIIIVICSGILKTLRCKNEKKRR 240
 DB 181 CGKEDSVVYCGPYFPGMNPFTIMNIIIGVLPIIIVICSGILKTLRCKNEKKRR 240

QY 241 AVRVIPTIMIVFLFWPTPNIVILNTFOEFGLSNCESTSQLDQATQVTEITLGMTHCCI 300
 DB 241 AVRVIPTIMIVFLFWPTPNIVILNTFOEFGLSNCESTSQLDQATQVTEITLGMTHCCI 300
 QY 301 NPITIAFVGEKRRSLFHIALGRIAPLQKPVCGPGVPRGKVKVKTTOGLDGRGKSKI 360
 DB 301 NPITIAFVGEKRRSLFHIALGRIAPLQKPVCGPGVPRGKVKVKTTOGLDGRGKSKI 360

RESULT 3

A43113
 chemokine (C-C) receptor 5 - human
 N:Alternate names: C-C CR-5; CCR5
 C:Species: Homo sapiens (man)
 C>Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #ext_change 20-Jun-2000
 C:Accession: A43113; S71808; A58834; A58832; G02653; A58833
 R:Samson, M.; Labbe, O.; Mollereau, C.; Vassart, G.; Parmentier, M.
 Biochemistry 35, 3362-3367, 1996
 A>Title: Molecular cloning and functional expression of a new human CC-chemokine recepto
 A:Reference number: A43113; MUID:96241590; PMID:8639485
 A:Accession: A43113
 A:Molecule type: mRNA
 A:Residues: 1-352 <SAM1>
 A:Cross-references: GB:X91492; NID:G1262810; PID:CAA62796.1; PID:G1262811
 R:Samson, M.; Libert, F.; Doranz, B.J.; Rucker, J.; Lienard, C.; Farber, C.M.; Saragost
 M.; Imai, T.; Rana, S.; Yi, Y.; Smyth, R.J.; Collman, R.G.; Doms, R.W.; Vassart, G.; Pa
 Nature 382, 722-725, 1996
 A>Title: Resistance to HIV-1 infection in caucasian individuals bearing mutant alleles o
 A:Reference number: S71808; MUID:9645670; PMID:8751444
 A:Accession: S71808
 A:Status: nucleic acid sequence not shown; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 182-206/207-230 <SAM2>
 A:Accession: A58834
 A:Status: nucleic acid sequence not shown; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-184; 'IKSHLGGAGPAACHGLILGNPKNSASVK' <SAM3>
 A:Cross-references: GB:X9393; NID:G1524062; PID:CAA67767.1; PID:G1524063
 A>Note: this frameshift mutation results in a non-functional receptor but confers a deg
 nd may have had a selective advantage by conferring resistance to Yersinia plague infect
 R:Combadiere, C.; Ahuja, S.K.; Tiffany, H.L.; Murphy, P.M.
 U. Leukoc. Biol. 60, 147-152, 1996
 A>Title: Cloning and functional expression of CC CKR5, a human monocyte CC chemokine rec
 A:Reference number: A58832; MUID:96295970; PMID:8699119
 A:Accession: A58832
 A:Molecule type: mRNA
 A:Residues: 1-352 <COM1>
 A:Cross-references: GB:U57840; NID:G1502408; PID:AA017071.1; PID:G1502409
 A:Experimental source: clone 8, endotoxin-stimulated peripheral blood monocytes
 R:Combadiere, C.
 submitted to the EMBL Data Library, May 1996
 A:Reference number: H01541
 A:Accession: G02653
 A:Status: translated from GB/EMBL/DDBJ
 A:Molecule type: mRNA
 A:Residues: 1-89; 'L', '91-352 <COM2>
 A:Cross-references: EMBL:U57840
 R:Raport, C.J.; Gosling, J.; Schweickart, V.L.; Gray, P.W.; Charo, I.F.
 J. Biol. Chem. 271, 17161-17166, 1996
 A>Title: Molecular cloning and functional characterization of a novel human CC chemokine
 A:Reference number: A58833; MUID:96291862; PMID:8663314
 A:Accession: A58833
 A:Molecule type: mRNA
 A:Residues: 1-352 <RAP>
 A:Cross-references: GB:U54994; NID:G1457945; PID:AA050598.1; PID:G1457946
 C:Comment: This is a receptor for chemokines MIP-1alpha (see PIR:A50574), MIP-1beta (see
 C:Genetics: Macrophage- and dual-tropic strains of HIV-1 bind to a complex of chemokine (C
 C:Gene: GDB:CMKBR5; CCR5; CR-5; CC-CR-5; CCR5; ChemR13
 A:Map position: 3p21-3p21
 C:function:
 A:Description: G protein-coupled receptor for chemokines MIP-1alpha, MIP-1beta and RANP-

RL Submitted (SEP-2002) to the EMBL/Genbank/DBJ databases.
 [6]
 RN SULFATION OF TYR-26, AND N-GLYCOSYLATION.
 RP MEDLINE=20501139; PubMed=11046064;
 RA Predezhnensky A.A., Dragan S., Kawano T., Gavrilin M.A., Gulina I.V.,
 RA Chetrazhensky L., Koliatukudy P.E.;
 RT "Monocytic chemotactic protein-1 receptor CCR2B is a glycoprotein that
 RT has tyrosine sulfation in a conserved extracellular N-terminal
 RT region.";
 RT J. Immunol. 165:5295-5303 (2000).
 CC -|- FUNCTION: Receptor for the MCP-1, MCP-3 and MCP-4 chemokines.
 CC Transduces a signal by increasing the intracellular calcium ions
 CC level. Alternative coreceptor with CD4 for HIV-1 infection.
 CC -|- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -|- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=A;
 CC IsoId=PA1597-1; Sequence=Displayed;
 CC Name=B;
 CC IsoId=PA1597-2; Sequence=VSP_001893;
 CC -|- PTM: N-glycosylated.
 CC -|- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL, U03882; AAA19119.1; -
 DR EMBL, U03905; AAA19120.1; -
 DR EMBL, D29984; BAA06253.1; -
 DR EMBL, U80924; AAC1637.1; -
 DR EMBL, U80924; AAC1636.1; -
 DR EMBL, U95626; AAB57791.1; -
 DR EMBL, U95626; AAB57792.1; -
 DR EMBL, AF545480; AAN16400.1; -
 DR PIR, J38450; J38450.
 DR PIR, J38443; J38443.
 DR PDB, 1KAD; Model; A=1-349.
 DR PDB, 1KPI; Model; A=1-349.
 DR GenB; HGNC:1603; CCR2.
 DR MIM; 601267; -
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0005625; C:soluble fraction; TAS.
 DR GO; GO:0004950; F:chemokine receptor activity; TAS.
 DR GO; GO:0019735; F:antimicrobial humoral response (sensu Verte. . .); TAS.
 DR GO; GO:0006968; P:cellular defense response; TAS.
 DR GO; GO:0006935; P:chemotaxis; TAS.
 DR GO; GO:0007204; P:cytosolic calcium ion concentration elevation; TAS.
 DR GO; GO:0006954; P:inflammatory response; TAS.
 DR GO; GO:0007259; P:JAK-STAT cascade; TAS.
 DR GO; GO:0007194; P:negative regulation of adenylate cyclase ac. . .; TAS.
 DR InterPro; IPR002237; CC_2 receptor.
 DR InterPro; IPR000355; Chemkin receptor.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCR_RHODOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
 DR 3D-structure; Alternative splicing; G-protein coupled receptor;
 KW Glycoprotein; Polymorphism; Sulfation; Transmembrane.
 FT DOMAIN 1 42 Extracellular (Potential).
 FT TRANSMEM 43 70 1 (Potential).
 FT DOMAIN 71 80 Cytoplasmic (Potential).
 FT TRANSMEM 81 100 2 (Potential).
 FT DOMAIN 101 114 Extracellular (Potential).
 FT TRANSMEM 115 136 3 (Potential).
 FT DOMAIN 137 153 Cytoplasmic (Potential).
 FT TRANSMEM 154 178 4 (Potential).
 FT DOMAIN 179 206 Extracellular (Potential).

FT TRANSMEM 207 226 5 (Potential).
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 FT TRANSMEM 244 268 6 (Potential).
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 FT TRANSMEM 286 309 7 (Potential).
 FT DOMAIN 310 374 Cytoplasmic (Potential).
 FT CAROXYD 14 14 N-linked (GlcNAc. . .) (Potential).
 FT MOD RES 26 26 Sulfotyrosine.
 FT DISULFID 113 190 By similarity.
 FT VARSPLIC 314 374 SLFHALGCRIALQKPCVGGVGRGKVKVKTGGLDGR
 GKGKSGRAPASLQDXEGA -> RYLSVFRKHTTKRCK
 QCVFRRFRTVDGVSTINPSTGQSVASGL (in
 isoform B).
 FT VARIANT 64 64 /FTId=VSP_001893.
 FT VARIANT 64 64 V -> I (in dbSNP:1799864).
 FT VARIANT 355 355 /FTId=VAR_014339.
 FT VARIANT 355 355 G -> E.
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 Query Match 100.0%; Score 1970; DB 1; Length 374;
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 Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 M L S T S R S R F I R N T N S G E V T T F P D Y D G A P C H K F D V Q I G A Q L L P P L Y S L V F I G F V G N 60
 DB 1 M L S T S R S R F I R N T N S G E V T T F P D Y D G A P C H K F D V Q I G A Q L L P P L Y S L V F I G F V G N 60
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 QY 241 A V R V I F T I M Y F L F W T P Y N I V I L N T R O E P F G S N C S T S Q L D A T O V T E L G M T H C C I 300
 DB 241 A V R V I F T I M Y F L F W T P Y N I V I L N T R O E P F G S N C S T S Q L D A T O V T E L G M T H C C I 300
 QY 301 N P I I A F Y G E K F R S I F H I A L G R I A P L Q P V C G G P G V R P G K V K Y T T O G L D G R G K G S I 360
 DB 301 N P I I A F Y G E K F R S I F H I A L G R I A P L Q P V C G G P G V R P G K V K Y T T O G L D G R G K G S I 360
 QY 361 G R A P A S L Q D X E G A 374
 DB 361 G R A P A S L Q D X E G A 374
 RESULT 2
 CCR2_MACMU STANDARD; PRT; 360 AA.
 ID CCR2_MACMU
 AC 018793;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE C-C chemokine receptor type 2 (C-C CKR-2) (CC-CCR-2) (CCR-2) (CCR2)
 DE (Monocyte chemoattractant protein 1 receptor) (MCP-1-R).
 GN Name=CCR2; Synonyms=CMKBR2;
 OS Macaca mulatta (rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 OC NCBI_TaxID=9544;
 RN NCBI_TaxID=9544;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21354176; PubMed=11461684; DOI=10.1089/089822201750290104;
 RA Margulies B.J., Hauer D.A., Clements J.E.;
 RT "Identification and comparison of eleven rhesus macaque chemokine

Db 61 MLVVLILNCKKLKCLTDIYLNLAIISDLLFLITPLMAHSAANEWFGNAMCKLFTGLY 120
QY 121 HIGYEGGIFFIILLTIDRYLAIVHAFALKARTVFGVTSVTWLVAVFASVPGIIFPK 180
Db 121 HIGYEGGIFFIILLTIDRYLAIVHAFALKARTVFGVTSVTWLVAVFASVPGIIFPK 180
QY 181 COKEDSVYVCGPYFPRGMNPFHTIMRNILGLVPLIMVICYSGILKTLRCRNEKRRR 240
Db 181 COKEDSVYVCGPYFPRGMNPFHTIMRNILGLVPLIMVICYSGILKTLRCRNEKRRR 240
QY 241 AVRVIFTIMIVYFLFTPNYIVILNTFOEFGLSNCESTSQLDQATQVTEITGMTHCCI 300
Db 241 AVRVIFTIMIVYFLFTPNYIVILNTFOEFGLSNCESTSQLDQATQVTEITGMTHCCI 300
QY 301 NPIIYAFVGEKRSFLHIALGRIAPLOKPVCGSGVPRGKVKVTTQGLDGRGKXSI 360
Db 301 NPIIYAFVGEKRSFLHIALGRIAPLOKPVCGSGVPRGKVKVTTQGLDGRGKXSI 360
QY 361 GRAPEASLQDKEGA 374
Db 361 GRAPEASLQDKEGA 374

RESULT 2
US-10-039-659-14
; Sequence 14, Application US/10039659
; Publication No. US20030018167A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Wei
; Gish, Kurt C.
; Schall, Thomas J.
; Vicari, Alain P.
; Zlotnik, Albert
; TITLE OF INVENTION: MAMMALIAN CHEMOKINE REAGENTS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/039,659
; FILING DATE: 03-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/887,977
; FILING DATE: 03-JUL-1997
; APPLICATION NUMBER: US 60/021,644
; FILING DATE: 05-JUL-1996
; APPLICATION NUMBER: US 60/028,329
; FILING DATE: 11-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0589K1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-852-9192
; TELEFAX: 650-496-1200
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 374 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-039-659-14

Query Match 100.0%; Score 1970; DB 14; Length 374;
Best Local Similarity 100.0%; Pred. No. 3.7e-163;
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLSTSRSPFIRNTNSGSEVTTFFPDYDGAPCHKFDVKQIGQLPPLYSLVIFFGVFN 60
Db 1 MLSTSRSPFIRNTNSGSEVTTFFPDYDGAPCHKFDVKQIGQLPPLYSLVIFFGVFN 60
QY 61 MLVVLILNCKKLKCLTDIYLNLAIISDLLFLITPLMAHSAANEWFGNAMCKLFTGLY 120
Db 61 MLVVLILNCKKLKCLTDIYLNLAIISDLLFLITPLMAHSAANEWFGNAMCKLFTGLY 120
QY 121 HIGYEGGIFFIILLTIDRYLAIVHAFALKARTVFGVTSVTWLVAVFASVPGIIFPK 180
Db 121 HIGYEGGIFFIILLTIDRYLAIVHAFALKARTVFGVTSVTWLVAVFASVPGIIFPK 180
QY 181 COKEDSVYVCGPYFPRGMNPFHTIMRNILGLVPLIMVICYSGILKTLRCRNEKRRR 240
Db 181 COKEDSVYVCGPYFPRGMNPFHTIMRNILGLVPLIMVICYSGILKTLRCRNEKRRR 240
QY 241 AVRVIFTIMIVYFLFTPNYIVILNTFOEFGLSNCESTSQLDQATQVTEITGMTHCCI 300
Db 241 AVRVIFTIMIVYFLFTPNYIVILNTFOEFGLSNCESTSQLDQATQVTEITGMTHCCI 300
QY 301 NPIIYAFVGEKRSFLHIALGRIAPLOKPVCGSGVPRGKVKVTTQGLDGRGKXSI 360
Db 301 NPIIYAFVGEKRSFLHIALGRIAPLOKPVCGSGVPRGKVKVTTQGLDGRGKXSI 360
QY 361 GRAPEASLQDKEGA 374
Db 361 GRAPEASLQDKEGA 374

RESULT 3
US-10-239-423-63
; Sequence 63, Application US/10239423
; Publication No. US20030186889A1
; GENERAL INFORMATION:
; APPLICANT: FORSSMANN, Wolf-Georg; FORSSMANN, Ulf; ADERMAN, Knut;
; HEITLAND, Aleksandra; SPODSBERG, Nikolaj
; TITLE OF INVENTION: Diagnostic Agent and Medicament for Examining the
; TITLE OF INVENTION: Cell Surface Proteome of Tumor and Inflammation Cells and
; TITLE OF INVENTION: for Treating Tumor Diseases and Inflammatory Diseases,
; TITLE OF INVENTION: Preferably with the Aid of Specific Chemokine
; TITLE OF INVENTION: Receptor Analysis and Chemokine Receptor/Ligand Interaction
; FILE REFERENCE: 022217u8
; CURRENT APPLICATION NUMBER: US/10/239,423
; CURRENT FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: DE10016013.1
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: Patentin Ver. 2.1
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Amino Acid Sequence for the Generation of Antibodies
US-10-239-423-63

Query Match 100.0%; Score 1970; DB 14; Length 374;
Best Local Similarity 100.0%; Pred. No. 3.7e-163;
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLSTSRSPFIRNTNSGSEVTTFFPDYDGAPCHKFDVKQIGQLPPLYSLVIFFGVFN 60
Db 1 MLSTSRSPFIRNTNSGSEVTTFFPDYDGAPCHKFDVKQIGQLPPLYSLVIFFGVFN 60
QY 61 MLVVLILNCKKLKCLTDIYLNLAIISDLLFLITPLMAHSAANEWFGNAMCKLFTGLY 120